

Met	Asp	Trp	Pro	His	Asn	Leu	Leu	Phe	Leu	Leu	Thr	Ile	Ser	Ile
1					5						10			15
Phe	Leu	Gly	Leu	Gly	Gln	Pro	Arg	Ser	Pro	Lys	Ser	Lys	Arg	Lys
					20					25			30	
Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val
					35					40			45	
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
					50					55			60	
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
					65					70			75	
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
					80					85			90	
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
					95					100			105	
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
					110					115			120	
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
					125					130			135	
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
					140					145			150	
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
					155					160			165	
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
					170					175			180	

FIGURE 1

aggcgggcag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50
cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300
acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
agcatcaacc acgacccccag ccgtatcccc gtggacctgc cggaggcacf 400
gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450
gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgcgcctc 500
tgccccccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550
gaccatcgct gtgggctgca cctgcattt ctgaatcacc tggcccagaa 600
gccaggccag cagccccaga ccattccct tgcacctttg tgccaagaaa 650
ggcctatgaa aagtaaacac tgactttga aagcaag 687

FIGURE 2

Met	Thr	Leu	Leu	Pro	Gly	Leu	Leu	Phe	Leu	Thr	Trp	Leu	His	Thr
1														15
Cys	Leu	Ala	His	His	Asp	Pro	Ser	Leu	Arg	Gly	His	Pro	His	Ser
					20				25					30
His	Gly	Thr	Pro	His	Cys	Tyr	Ser	Ala	Glu	Glu	Leu	Pro	Leu	Gly
					35				40					45
Gln	Ala	Pro	Pro	His	Leu	Leu	Ala	Arg	Gly	Ala	Lys	Trp	Gly	Gln
					50				55					60
Ala	Leu	Pro	Val	Ala	Leu	Val	Ser	Ser	Leu	Glu	Ala	Ala	Ser	His
					65				70					75
Arg	Gly	Arg	His	Glu	Arg	Pro	Ser	Ala	Thr	Thr	Gln	Cys	Pro	Val
					80				85					90
Leu	Arg	Pro	Glu	Glu	Val	Leu	Glu	Ala	Asp	Thr	His	Gln	Arg	Ser
					95				100					105
Ile	Ser	Pro	Trp	Arg	Tyr	Arg	Val	Asp	Thr	Asp	Glu	Asp	Arg	Tyr
					110				115					120
Pro	Gln	Lys	Leu	Ala	Phe	Ala	Glu	Cys	Leu	Cys	Arg	Gly	Cys	Ile
					125				130					135
Asp	Ala	Arg	Thr	Gly	Arg	Glu	Thr	Ala	Ala	Leu	Asn	Ser	Val	Arg
					140				145					150
Leu	Leu	Gln	Ser	Leu	Leu	Val	Leu	Arg	Arg	Arg	Pro	Cys	Ser	Arg
					155				160					165
Asp	Gly	Ser	Gly	Leu	Pro	Thr	Pro	Gly	Ala	Phe	Ala	Phe	His	Thr
					170				175					180
Glu	Phe	Ile	His	Val	Pro	Val	Gly	Cys	Thr	Cys	Val	Leu	Pro	Arg
					185				190					195
Ser	Val													
		197												

FIGURE 3

gccaggtgtg caggccgctc caagcccagc ctgccccgct gccgccacca 50
tgacgctcct cccccggcctc ctgtttctga cctggctgca cacatgcctg 100
gcccaccatg acccctccct cagggggcac ccccacagtc acggtacccc 150
acactgctac tcggctgagg aactgcccct cggccaggcc ccccccacacc 200
tgctggctcg aggtgccaag tgggggcagg ctttgcctgt agccctggtg 250
tccagcctgg aggcaag ccacaggggg aggcacgaga ggcctcagc 300
tacgacccag tgcccggtgc tgccggccgga ggaggtgttg gaggcagaca 350
cccaccagcg ctccatctca ccctggagat accgtgtgga cacggatgag 400
gaccgctatac cacagaagct ggcattcgcc gagtgccctgt gcagaggctg 450
tatcgatgca cggacgggcc gcgagacagc tgcgctcaac tccgtgcggc 500
tgctccagag cctgctggtg ctgcggccgc ggcctgctc ccgcgacggc 550
tcggggctcc ccacacctgg ggccttgcc ttccacacccg agttcatcca 600
cgtccccgtc ggctgcacct gcgtgctgcc ccgttcagtg tgaccgcccga 650
ggccgtgggg cccctagact ggacacgtgt gctccccaga gggcacccccc 700
tatttatgtg tatttattgt tatttatatg cctcccccaa cactaccctt 750
gggtctggg cattccccgt gtctggagga cagccccca ctgttctcct 800
catctccagc ctcagtagtt ggggttagaa ggagctcagc acctttcca 850
gcccttaaag ctgcagaaaa ggtgtcacac ggctgcctgt accttggctc 900
cctgtcctgc tcccggttc cttacccta tcactggct caggccccgc 950
aggctgcctc ttcccaacct ctttggaaat acccctgttt cttaaacaat 1000
tatattaagtg tacgtgtatt attaaactga tgaacacatc cccaaaa 1047

FIGURE 4

ggcagcagg accaagagag gcacgcttgc ccttttatga catcagagct 50
cctggttctt gctccttggg actctggac ttacaccagt ggcacccctg 100
gctcnnnnnn nnnnnaattc ggtacgaggc tggggttcag gcgggcagca 150
gctgcaggct gaccttgcag cttggcgaa tggactggcc tcacaacctg 200
ctgtttcttc ttaccatttc catcttcctg gggctggcc agcccaggag 250
ccccaaaagc aagaggaagg ggcaaggcg gcctgggcc ctggtccctg 300
gccctcacca ggtgccactg gacctggtgt cacggatgaa accgtatgcc 350
cgcatggagg agtatgagag gaacatcgag gagatgttgg cccagctgag 400
gaacagttca gagctggccc agagaaagtg tgaggtcaac ttgcagctgt 450
ggatgtccaa caagaggagc ctgtctccct gggctacag catcaaccac 500
gaccccagcc gtatccccgt ggacctccgg aggacacggtg cctgtgtctg 550
ggcttgtgtg aacccttca ccatgcagga ggaccgcagc atggtgagcg 600
tgccggtgtt cagccaggtt cctgtgcgcc gccgcctctg cccgccaccg 650
ccccgcacag ggccttgccg ccagcgcgca gtcatggaga ccatcgctgt 700
gggctgcacc tgcacatcttct gaatcgacct ggcccagaag ccaggccagc 750
agcccagac catcctcctt gcaccttgcgt gccaagaaag gcctatgaaa 800
agtaaacact gactttgaa agcaaaaaaa 830

FIGURE 5

cacggatgag gaccgctatac cacagaagct ggccttcgcc gagtgccctgt 50
gcagaggctg tatcgatgca cggacgggcc gcgagacagc tgcgctcaac 100
tccgtgcggc tgctccagag cctgctggtg ctgcgcccgc ggccttgctc 150
ccgcgcacggc tcggggctcc ccacacctgg ggccttgcc ttccacacccg 200
agttcatcca cgtccccgtc ggctgcacct 230

FIGURE 6

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FIGURE 7A

Tue Apr 27 16:58:30 1999
/home/ruby/va/Molbio/carpenda/temp/aa.out

59294	1	[MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGP---HQVPL]
62377	1	[MTLLPGLLFLLTWLHTCLAHHDPS-SLRGHPHSHGTPHCYSAEELPLGQAPP]
59294	48	[DLIVSRMKPYARM--EYEYERNIEEMVAQLRNSSEL[QRKCEV----NLQLW]
62377	50	[HLLARGAKWGQALPVAVSSLEASHRGHRERPSATTOCPVLRPEEVLEA]
59294	92	[MSNKRSLSPWGYSIINHDPSRI[PVDLPEARCLCLGCVNPFTMQEDRSMVSV]
62377	100	[DTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRIGCIDARTGRETAALNSV]
59294	142	[PVF-[SQVPVRRRLC]PPP----PRTGPCRQRRAVMETIAVGCTCIF]
62377	150	[RLLQSLLVLRRRP[C]SRDGSGLP[TPGAFAFHTEFIHVPGVGC[VLPRSV]

FIGURE 7B

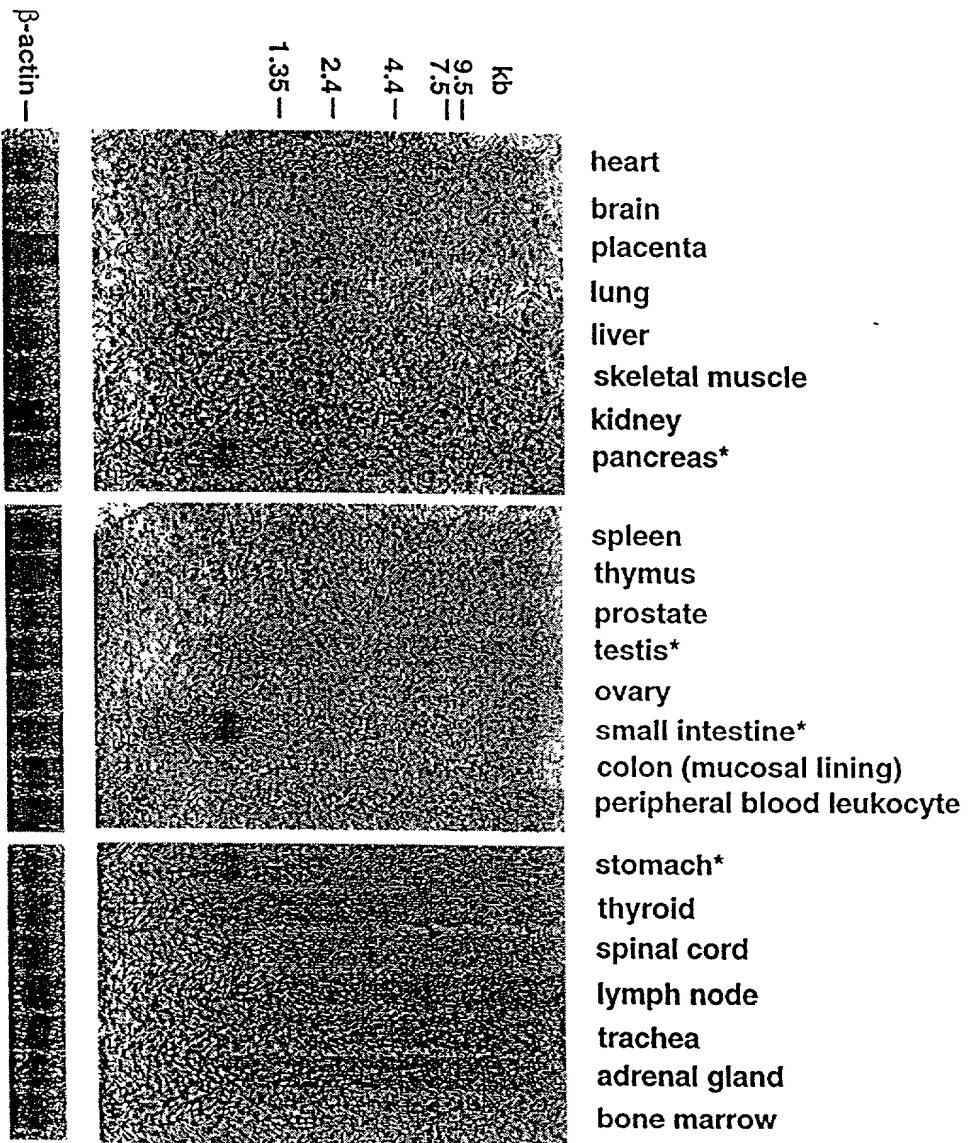
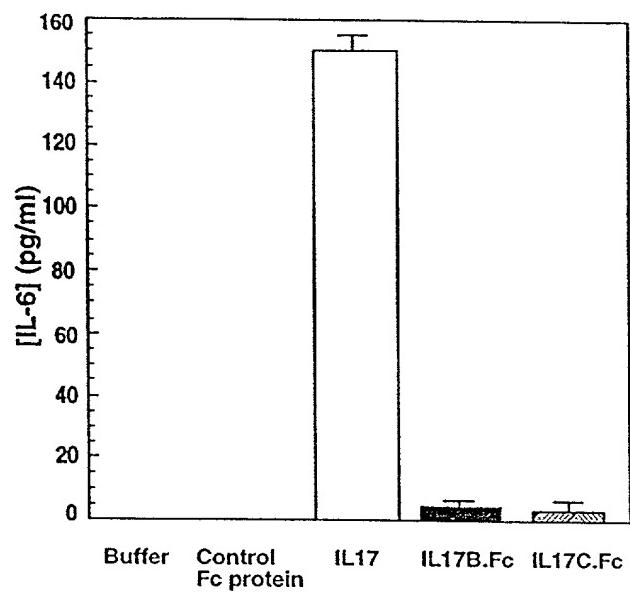


FIGURE 8

A. HFF cells



B. THP1 cells

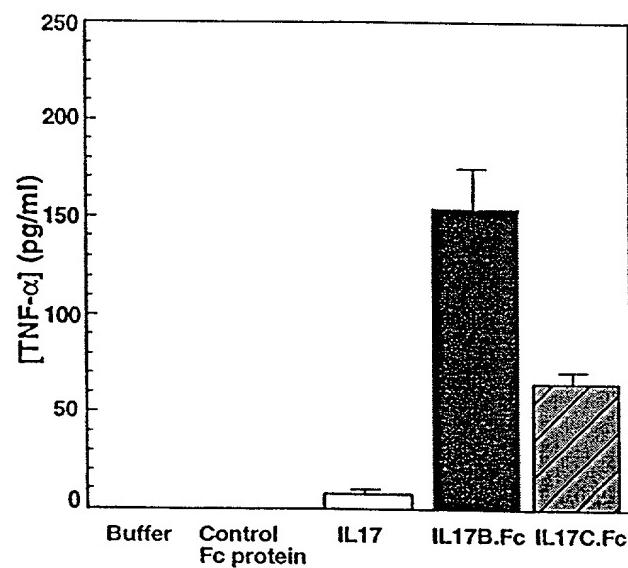
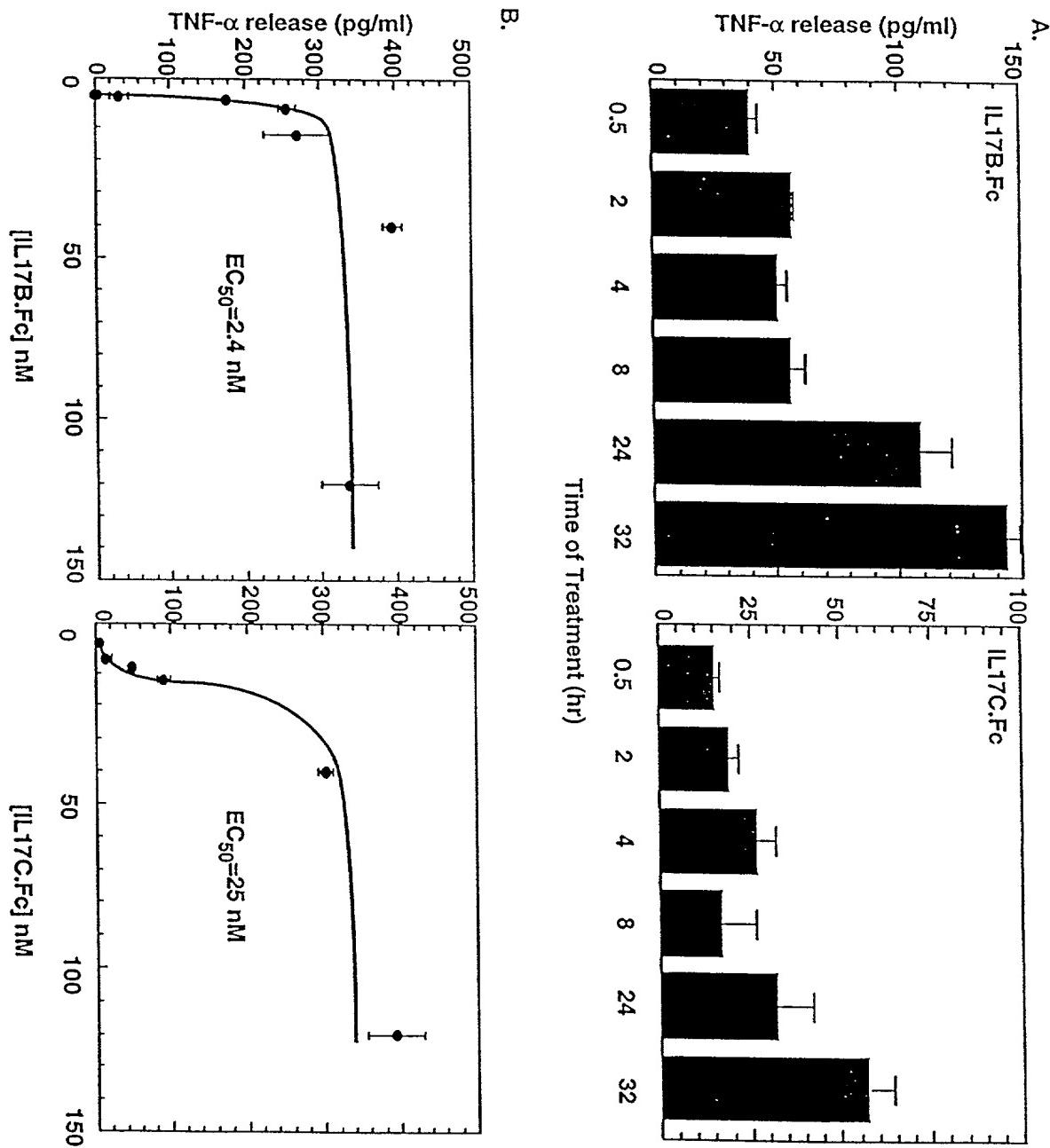


FIGURE 9

FIGURE 10



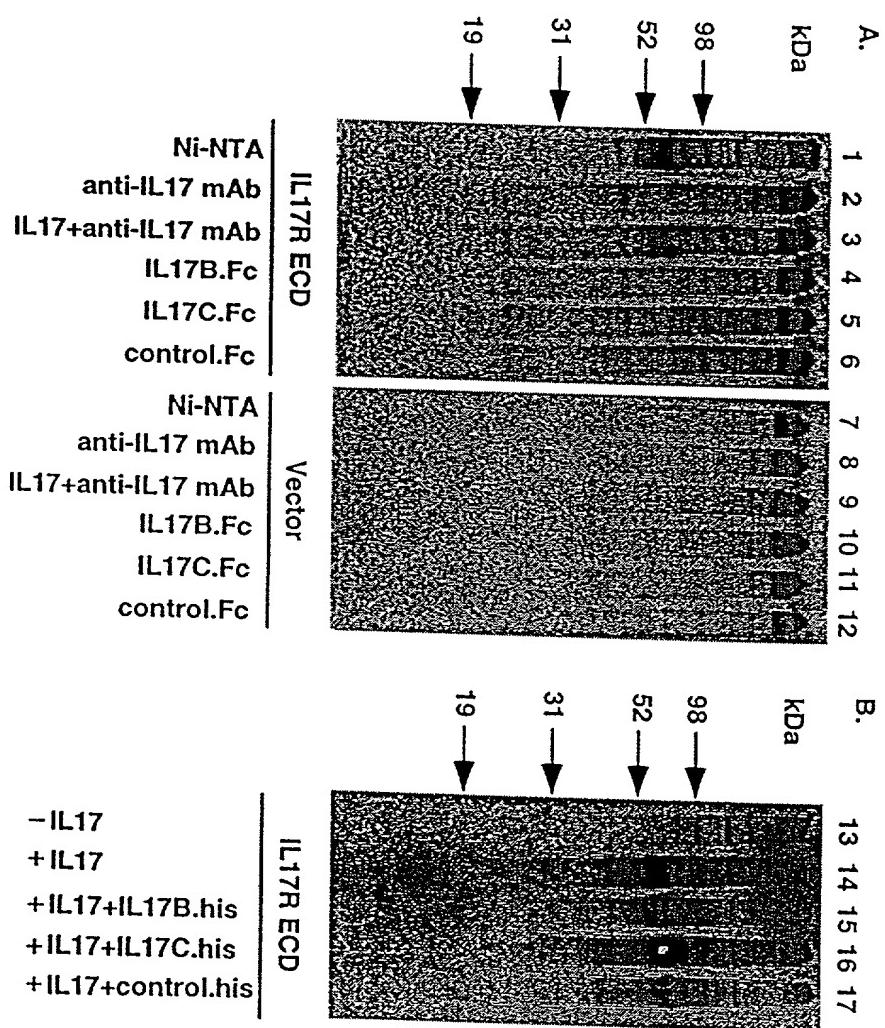


FIGURE 11

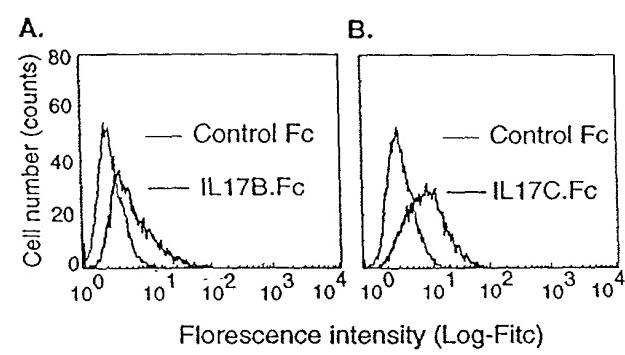


FIGURE 12

IL-17 induces breakdown and inhibits synthesis of cartilage matrix

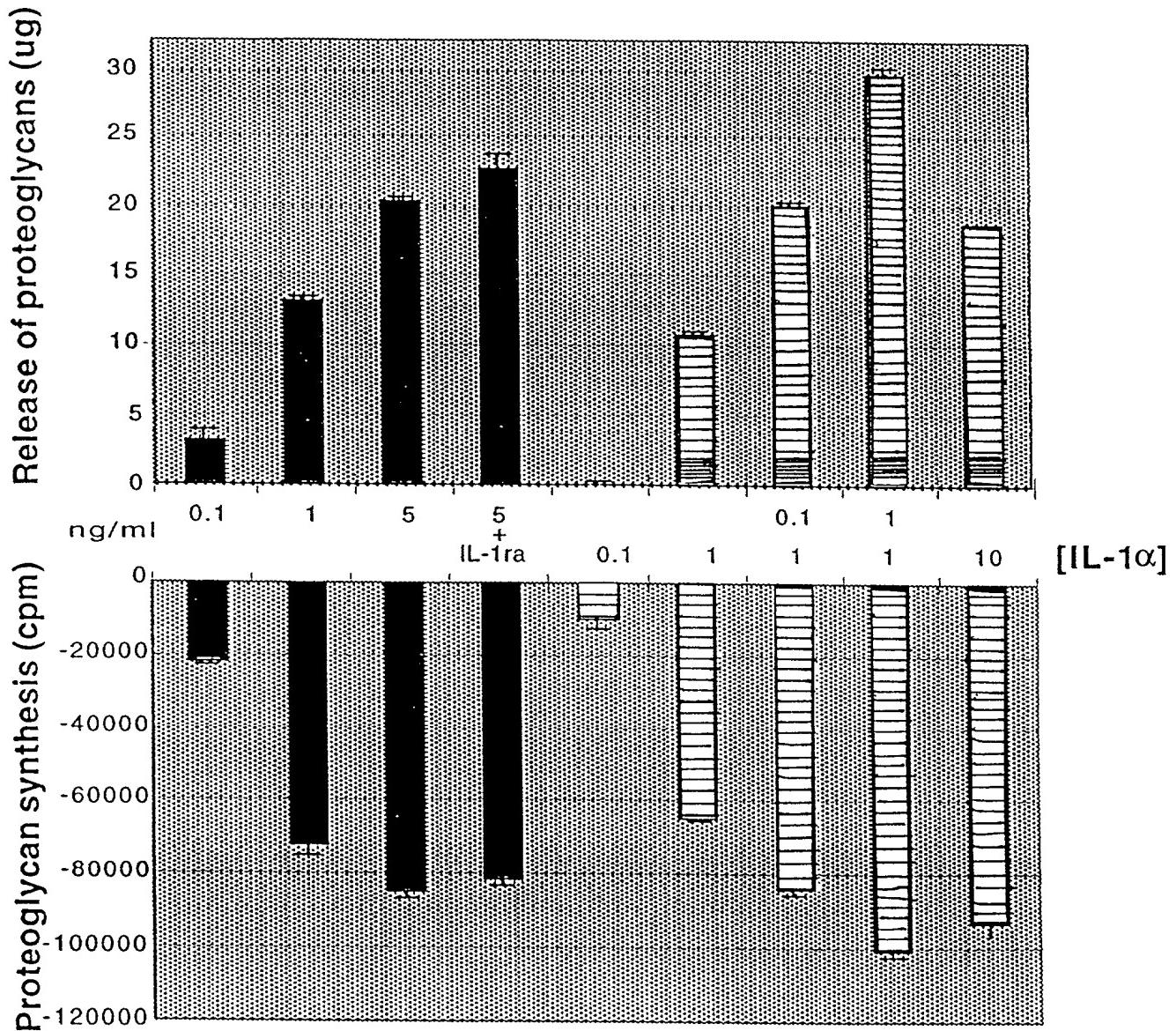


FIGURE 13

IL-17 increases basal and IL-1 α -induced nitric oxide release

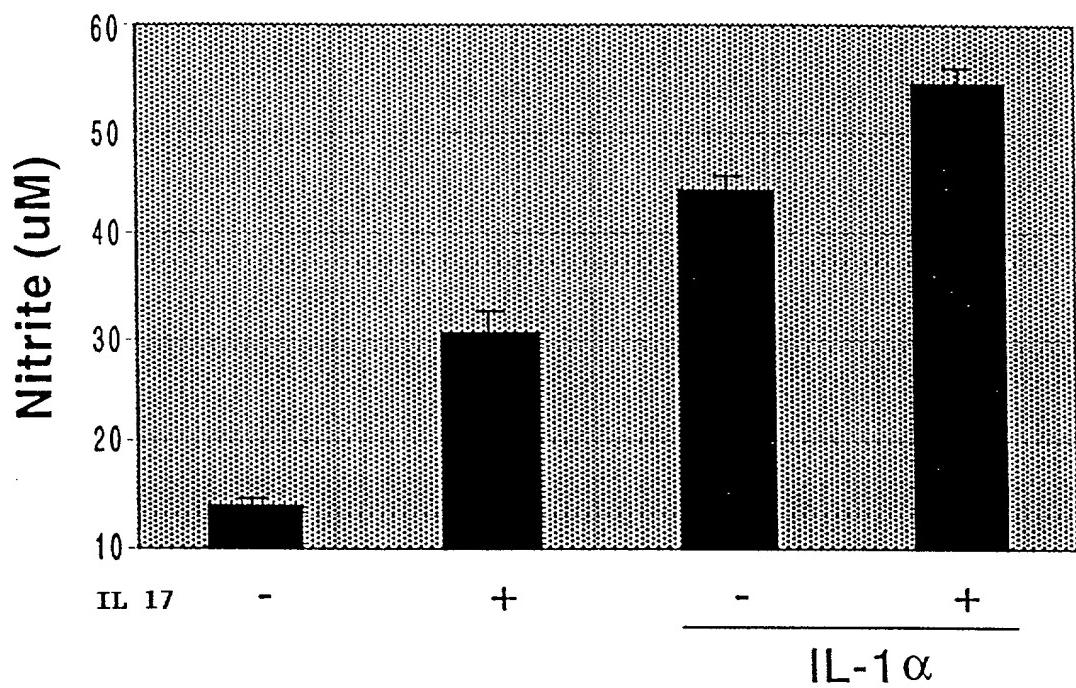
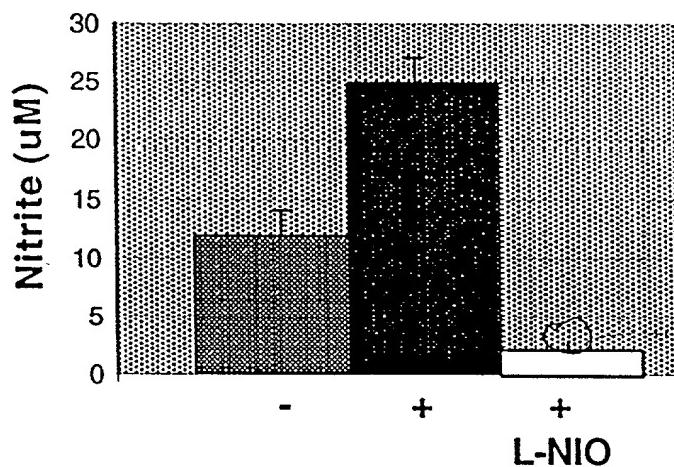


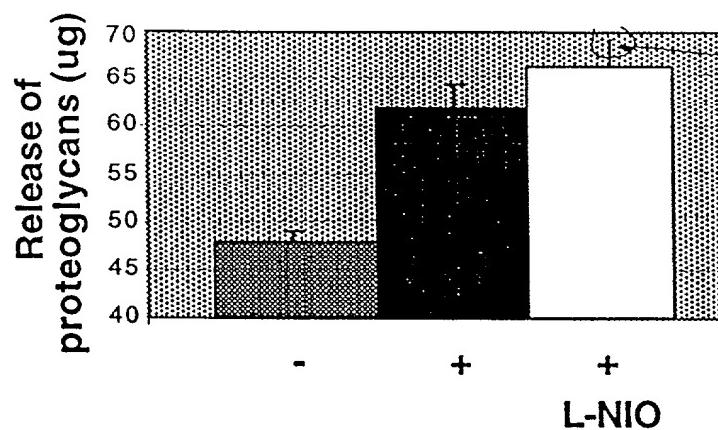
FIGURE 14

Inhibition of nitric oxide release does not block the detrimental effects of IL-1 β on matrix breakdown or synthesis

A.



B.



C.

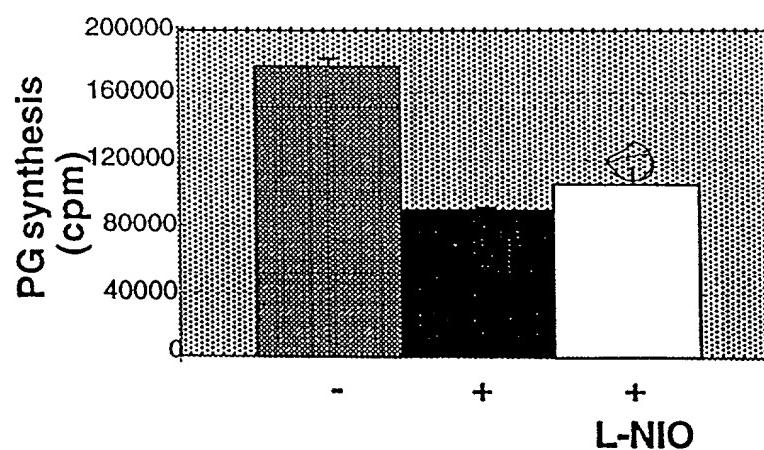


FIGURE 15

**INHIBITION of NO release enhances
IL1- α -induced matrix breakdown
but not matrix synthesis**

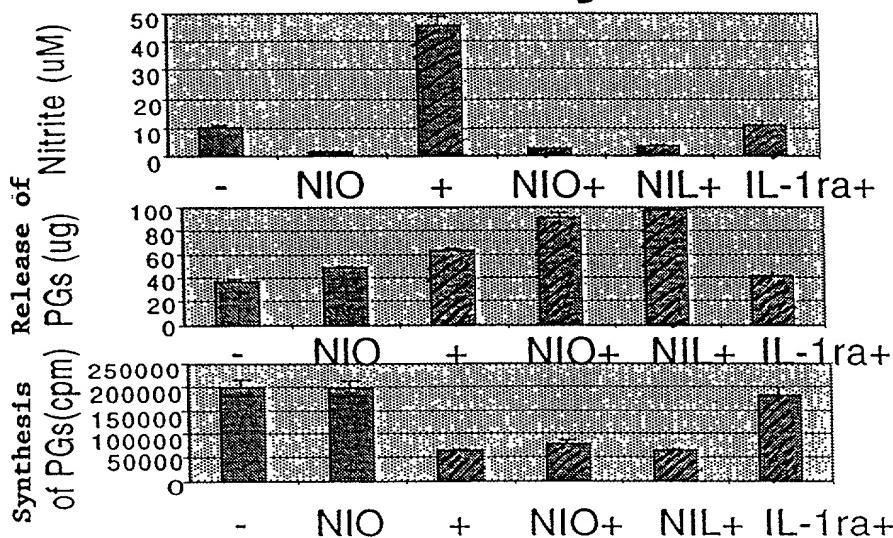


FIGURE 16

IL-17 homologue 1 (UNQ516)
has positive effects on
articular cartilage

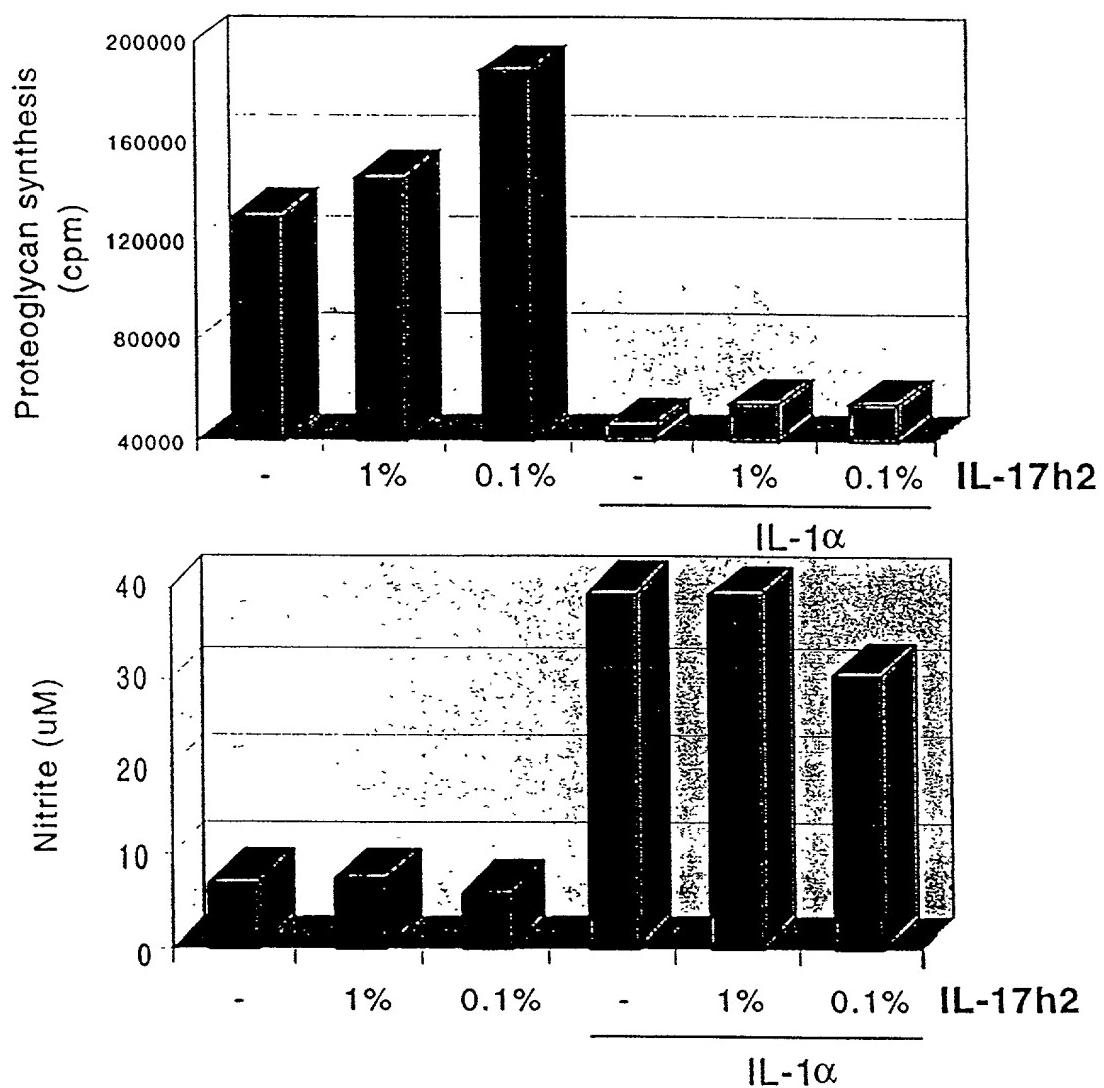


FIGURE 17

IL-17 homologue (UNQ 561) has detrimental effects on articular cartilage

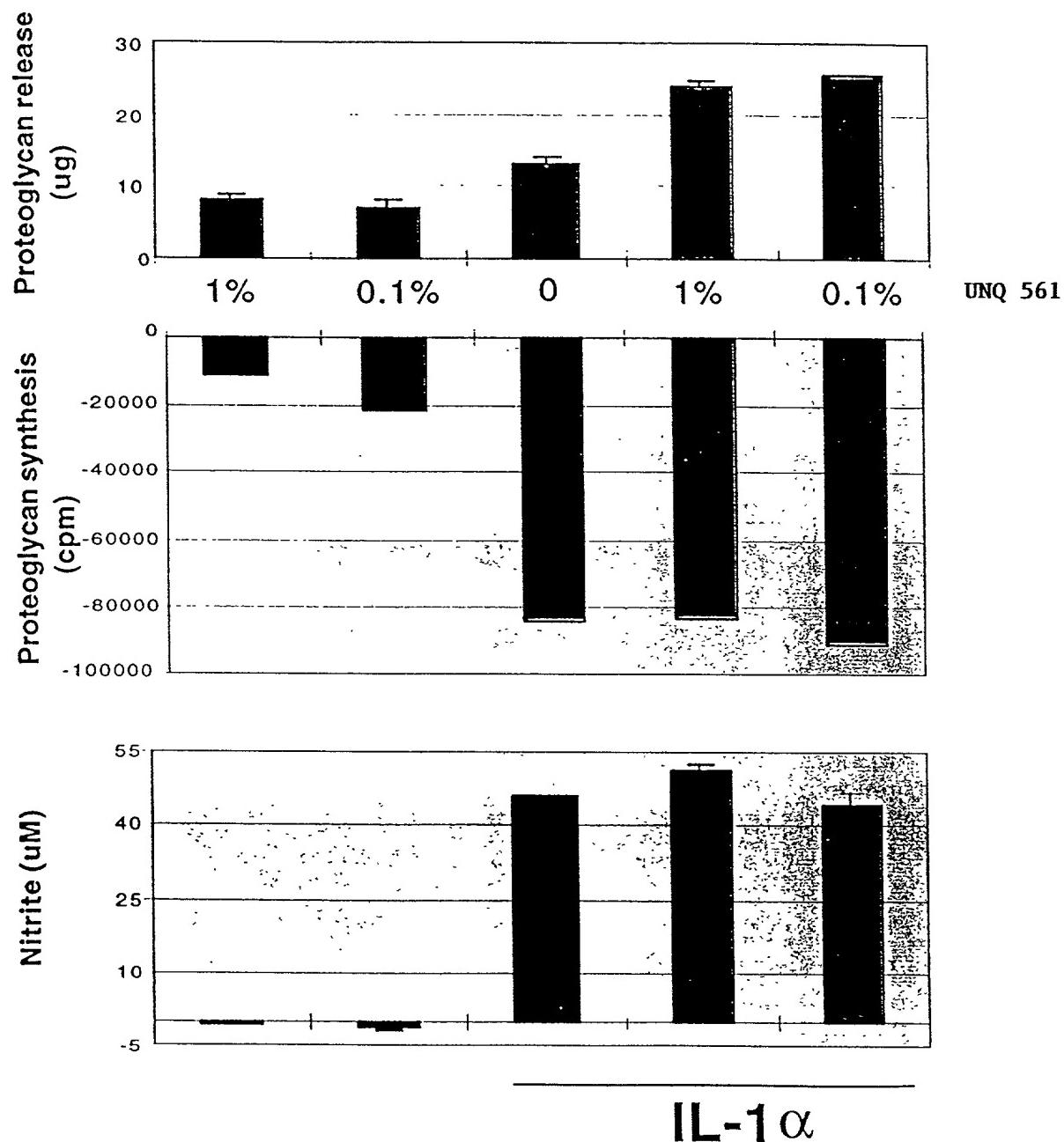


FIGURE 18